Library Seguence Search History
russel - 10 / 519524
Page 1

=> fil reg
FILE 'REGISTRY' ENTERED AT 07:56:20 ON 26 JUN 2006
USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT.
PLEASE SEE "HELP USAGETERMS" FOR DETAILS.
COPYRIGHT (C) 2006 American Chemical Society (ACS)

Property values tagged with IC are from the ZIC/VINITI data file provided by InfoChem.

STRUCTURE FILE UPDATES: 25 JUN 2006 HIGHEST RN 889359-45-9 DICTIONARY FILE UPDATES: 25 JUN 2006 HIGHEST RN 889359-45-9

New CAS Information Use Policies, enter HELP USAGETERMS for details.

TSCA INFORMATION NOW CURRENT THROUGH January 6, 2006

Please note that search-term pricing does apply when conducting SmartSELECT searches.

Structure search iteration limits have been increased. See HELP SLIMITS for details.

REGISTRY includes numerically searchable data for experimental and predicted properties as well as tags indicating availability of experimental property data in the original document. For information on property searching in REGISTRY, refer to:

http://www.cas.org/ONLINE/UG/regprops.html

=> d l1 sqide can tot

L1 ANSWER 1 OF 2 REGISTRY COPYRIGHT 2006 ACS on STN

RN 620973-82-2 REGISTRY

CN L-Glutamic acid, L-phenylalanyl-L-lysylglycyl-L- α -glutamyl-L-glutaminyl-L-alanyl-L-prolyl-L-lysylglycyl- (9CI) (CA INDEX NAME) OTHER NAMES:

CN 2: PN: CN1386754 SEQID: 2 claimed sequence

FS PROTEIN SEQUENCE; STEREOSEARCH

SQL 10

PATENT ANNOTATIONS (PNTE):

> |claimed |SEQID 2

SEQ 1 FKGEQAPKGE

HITS AT: 1-10

MF C48 H75 N13 O16

SR CA

LC STN Files: CA, CAPLUS, TOXCENTER

DT.CA CAplus document type: Journal; Patent

RL.P Roles from patents: BIOL (Biological study); PRP (Properties); USES

(Uses)

RL.NP Roles from non-patents: BIOL (Biological study); PRP (Properties)

Absolute stereochemistry.

PAGE 1-A

Ph
$$H_{2N}$$
 H_{2N} H_{2N}

PAGE 1-B

PROPERTY DATA AVAILABLE IN THE 'PROP' FORMAT

3 REFERENCES IN FILE CA (1907 TO DATE)

3 REFERENCES IN FILE CAPLUS (1907 TO DATE)

REFERENCE 1: 143:76700

REFERENCE 2: 140:281378

REFERENCE 3: 139:363392

L1 ANSWER 2 OF 2 REGISTRY COPYRIGHT 2006 ACS on STN

RN 211099-13-7 REGISTRY

CN L-Proline, L-alanylglycyl-L-phenylalanyl-L-lysylglycyl-L-α-glutamyl-L-glutaminyl-L-alanyl-L-prolyl-L-lysylglycyl-L-α-glutamyl- (9CI) (CA INDEX NAME)

FS PROTEIN SEQUENCE; STEREOSEARCH

SQL 13

SEQ 1 AGFKGEQAPK GEP

HITS AT: 3-12

MF C58 H90 N16 O19

SR CA

LC STN Files: CA, CAPLUS, TOXCENTER DT.CA CAplus document type: Journal

RL.NP Roles from non-patents: PRP (Properties)

Absolute stereochemistry.

PAGE 1-A

PAGE 2-A

$$\begin{array}{c|c} & & & & \\ & &$$

PROPERTY DATA AVAILABLE IN THE 'PROP' FORMAT

1 REFERENCES IN FILE CA (1907 TO DATE)

1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

REFERENCE 1: 129:160544

=> d his

(FILE 'HOME' ENTERED AT 07:53:39 ON 26 JUN 2006) SET COST OFF

FILE 'REGISTRY' ENTERED AT 07:54:09 ON 26 JUN 2006

E FKGEQAPKGE/SQEP

L1 2 S FKGEQAPKGE/SQSP

FILE 'HCAOLD' ENTERED AT 07:54:40 ON 26 JUN 2006

L2 0 S L1

FILE 'USPATFULL' ENTERED AT 07:54:46 ON 26 JUN 2006

L3 0 S L1

FILE 'HCAPLUS' ENTERED AT 07:54:49 ON 26 JUN 2006

L4 4 S L1

L5 3 S L4 AND LI Z?/AU

L6 1 S L4 AND (WO2003-CN496 OR CN2002-123412)/AP, PRN

L7 4 S L4-L6

FILE 'REGISTRY' ENTERED AT 07:56:20 ON 26 JUN 2006

=> fil hcaplus

FILE 'HCAPLUS' ENTERED AT 07:56:29 ON 26 JUN 2006
USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT.
PLEASE SEE "HELP USAGETERMS" FOR DETAILS.
COPYRIGHT (C) 2006 AMERICAN CHEMICAL SOCIETY (ACS)

Copyright of the articles to which records in this database refer is held by the publishers listed in the PUBLISHER (PB) field (available for records published or updated in Chemical Abstracts after December 26, 1996), unless otherwise indicated in the original publications. The CA Lexicon is the copyrighted intellectual property of the the American Chemical Society and is provided to assist you in searching databases on STN. Any dissemination, distribution, copying, or storing of this information, without the prior written consent of CAS, is strictly prohibited.

FILE COVERS 1907 - 26 Jun 2006 VOL 145 ISS 1 FILE LAST UPDATED: 25 Jun 2006 (20060625/ED)

New CAS Information Use Policies, enter HELP USAGETERMS for details.

This file contains CAS Registry Numbers for easy and accurate substance identification.

=> d 17 all hitstr tot

- L7 ANSWER 1 OF 4 HCAPLUS COPYRIGHT 2006 ACS on STN
- AN 2005:352633 HCAPLUS
- DN 143:76700
- ED Entered STN: 25 Apr 2005
- TI The inhibitory effect of altered collagen II peptide on HLA-DRB1-restricted T-cell activation
- AU Cheng, Y. J.; Zhou, Q.; Li, Z. G.
- CS Department of Rheumatology & Immunology, People's Hospital, Peking University Medical School, Beijing, Peop. Rep. China
- SO Scandinavian Journal of Immunology (2005), 61(3), 260-265 CODEN: SJIMAX; ISSN: 0300-9475
- PB Blackwell Publishing Ltd.
- DT Journal
- LA English
- CC 15-10 (Immunochemistry)
 Section cross-reference(s): 1
- AB It has been known that rheumatoid arthritis (RA)-associated antigenic peptides CII263-272 are coupled with human leukocyte antigen (HLA)-DRB1 and recognized by T-cell receptor (TCR), which in turn induced T-cell proliferation and pathogenesis of RA. Non-T-cell-stimulating type II collagen (CII) peptides might be generated by removing the amino acids responsible for TCR contact and keeping the HLA-DR-binding residues intact. In this study, a panel of altered CII peptides (APs) with consecutive or single substitutions of the TCR-contacting residues were Through peptide binding and T-cell activation assays, we synthesized. demonstrated that altered CII263-272 peptides with substitution of the TCR-contacting residues did not or barely induced T-cell activation; one of the best non-T-cell-stimulating peptide AP268-270 inhibited the binding of wild-type CII263-272 to HLA-DR1 and T-cell activation triggered by wild-type CII263-272 and HA306-318 in a dose-response manner. These data suggest that removal of the TCR-contacting residues of CII263-272 leads to HLA-DRB1 binding and low T-cell-stimulating peptides, which could potentially inhibit the T-cell response induced by HLA-DRB1-binding antigenic peptides.
- ST collagen II peptide T cell activation immunosuppression HLA
- IT Histocompatibility antigens
 - RL: BSU (Biological study, unclassified); BIOL (Biological study) (HLA-DRB1; inhibitory effect of altered collagen II peptide on HLA-DRB1-restricted T-cell activation)

```
IT
     Cell activation
        (T cell; inhibitory effect of altered collagen II peptide on
        HLA-DRB1-restricted T-cell activation)
IT
     T cell (lymphocyte)
        (activation; inhibitory effect of altered collagen II peptide on
        HLA-DRB1-restricted T-cell activation)
ΙT
     Human
     Immunosuppressants
     Immunosuppression
     MHC restriction
     Mutagenesis
        (inhibitory effect of altered collagen II peptide on
        HLA-DRB1-restricted T-cell activation)
ΙT
     TCR (T cell receptors)
     RL: BSU (Biological study, unclassified); BIOL (Biological study)
        (inhibitory effect of altered collagen II peptide on
        HLA-DRB1-restricted T-cell activation)
IΤ
     Peptides, biological studies
     RL: BSU (Biological study, unclassified); PAC (Pharmacological activity);
     BIOL (Biological study)
        (inhibitory effect of altered collagen II peptide on
        HLA-DRB1-restricted T-cell activation)
ΙT
     Rheumatoid arthritis
       (inhibitory effect of altered collagen II peptide on
        HLA-DRB1-restricted T-cell activation in relation to rheumatoid
        arthritis)
IT
     Collagens, biological studies
     RL: BSU (Biological study, unclassified); BIOL (Biological study)
        (type II; inhibitory effect of altered collagen II peptide on
        HLA-DRB1-restricted T-cell activation)
IT
     620973-80-0 620973-82-2
                               620973-84-4
                                             620973-86-6
     620973-87-7
     RL: BSU (Biological study, unclassified); PAC (Pharmacological activity);
     BIOL (Biological study)
        (inhibitory effect of altered collagen II peptide on
        HLA-DRB1-restricted T-cell activation)
              THERE ARE 25 CITED REFERENCES AVAILABLE FOR THIS RECORD
RE.CNT
RE
(1) Andersson, E; Proc Natl Acad Sci USA 1998, V95, P7574 HCAPLUS
(2) Brand, D; J Immunol 1994, V152, P3088 HCAPLUS
(3) Deighton, C; Ann Rheum Dis 1993, V52, P638 MEDLINE
(4) Dessen, A; Immunity 1997, V7, P473 HCAPLUS
(5) Diab, B; Immunogenetics 1999, V49, P36 HCAPLUS
(6) Fremont, D; Science 1996, V272, P1001 HCAPLUS
(7) Fridkis-Hareli, M; J Immunol 1998, V160, P4386 HCAPLUS
(8) Fridkis-Hareli, M; Proc Natl Acad Sci USA 1998, V95, P12528 HCAPLUS
(9) Fugger, L; Eur J Immunol 1996, V26, P928 HCAPLUS
(10) Goldring, S; Curr Rheumatol Rep 2002, V4, P226
(11) Gregersen, P; Arthritis Rheum 1987, V30, P1205 HCAPLUS
(12) Kim, H; Arthritis Rheum 1999, V42, P2085 HCAPLUS
(13) Nepom, G; Arthritis Rheum 1989, V32, P15 MEDLINE
(14) Nepom, G; Rheum Dis Clin North Am 2001, V27, P305 MEDLINE
(15) Ohta, N; Hum Immunol 1982, V5, P123 MEDLINE
(16) Prakken, B; Arthritis Rheum 2002, V46, P1937 HCAPLUS
(17) Rosloniec, E; Cell Immunol 1996, V172, P21 HCAPLUS
(18) Rosloniec, E; J Exp Med 1997, V185, P1113 HCAPLUS
(19) Rosloniec, E; J Immunol 2002, V168, P253 HCAPLUS
(20) Rosloniec, E; J Immunol 2002, V160, P2573
(21) Stern, L; Nature 1994, V368, P215 HCAPLUS
(22) Vergelli, M; Eur J Immunol 1996, V26, P2624 HCAPLUS
```

- (23) Zhou, Q; Chin J Rheumatol 2002, V6, P397
- (24) Zhou, Q; Chin J Rheumatol 2003, V7, P324
- (25) Zhou, Q; Hum Immunol 2003, V4(9), P857

IT 620973-82-2

RL: BSU (Biological study, unclassified); PAC (Pharmacological activity); BIOL (Biological study)

(inhibitory effect of altered collagen II peptide on

HLA-DRB1-restricted T-cell activation)

RN 620973-82-2 HCAPLUS

CN L-Glutamic acid, L-phenylalanyl-L-lysylglycyl-L- α -glutamyl-L-glutaminyl-L-alanyl-L-prolyl-L-lysylglycyl- (9CI) (CA INDEX NAME)

Absolute stereochemistry.

PAGE 1-B

- L7 ANSWER 2 OF 4 HCAPLUS COPYRIGHT 2006 ACS on STN
- AN 2003:958293 HCAPLUS
- DN 140:281378
- ED Entered STN: 09 Dec 2003
- TI Non-T lymphocyte binding peptides derived from collagen type II and uses in treating rheumatoid arthritis
- IN Li, Zhanguo

```
People's Hospital of Peking University, Peop. Rep. China
PA
SO
     Faming Zhuanli Shenqing Gongkai Shuomingshu, 20 pp.
     CODEN: CNXXEV
DT
     Patent
    Chinese
LA
     ICM C07K0014-435
IC
     ICS A61K0038-17; A61P0037-02; A61P0019-02
     1-7 (Pharmacology)
CC
     Section cross-reference(s): 15
FAN.CNT 1
    PATENT NO.
                        KIND
                               DATE
                                         APPLICATION NO.
                                                                DATE
     -----
                       ____
                               -----
                                          -----
    CN 1386754
                               20021225 CN 2002-123412 20020627 <-- 20040108 WO 2003-CN496 20030626 <--
    WO 2004003007
                       Α
PΙ
                       A
A1
        W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN,
            CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH,
            GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR,
            LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NI, NO, NZ, OM,
            PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT,
            TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW
        RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY,
            KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES,
            FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, SE, SI, SK, TR, BF,
            BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG
                                        AU 2003-280443
    AU 2003280443
                               20040119
                        A1
                                                                20030626 <--
    EP 1541583
                         Α1
                               20050615
                                         EP 2003-739970
                                                                 20030626 <--
            AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT,
            IE, SI, LT, LV, FI, RO, MK, CY, AL, TR, BG, CZ, EE, HU, SK
    JP 2006508901
                        Т2
                               20060316
                                         JP 2004-516425
                                                                20030626 <--
PRAI CN 2002-123412
                         Α
                               20020627
    WO 2003-CN496
                         W
                               20030626
                                        <--
CLASS
PATENT NO.
                CLASS PATENT FAMILY CLASSIFICATION CODES
-----
                       ______
                ----
CN 1386754
                ICM
                       C07K0014-435
                ICS
                       A61K0038-17; A61P0037-02; A61P0019-02
                IPCI
                       C07K0014-435 [ICM, 7]; A61K0038-17 [ICS, 7]; A61P0037-02
                       [ICS,7]; A61P0037-00 [ICS,7,C*]; A61P0019-02 [ICS,7];
                       A61P0019-00 [ICS,7,C*]
                IPCR
                       A61K0038-00 [N,A]; A61K0038-00 [N,C*]; C07K0007-00
                       [I,C*]; C07K0007-06 [I,A]
WO 2004003007
                IPCI
                       C07K0007-06 [ICM, 7]; C07K0007-00 [ICM, 7, C*];
                       A61K0038-08 [ICS,7]; A61P0019-02 [ICS,7]; A61P0019-00
                       [ICS,7,C*]; A61P0037-06 [ICS,7]; A61P0037-00 [ICS,7,C*]
                IPCR
                       A61K0038-00 [N,A]; A61K0038-00 [N,C*]; C07K0007-00
                       [I,C*]; C07K0007-06 [I,A]
                ECLA
                       C07K007/06A
AU 2003280443
                       C07K0007-06 [ICM,7]; C07K0007-00 [ICM,7,C*];
                IPCI
                       A61K0038-08 [ICS,7]; A61P0019-02 [ICS,7]; A61P0019-00
                       [ICS,7,C*]; A61P0037-06 [ICS,7]; A61P0037-00 [ICS,7,C*]
EP 1541583
                IPCI
                       C07K0007-06 [ICM,7]; C07K0007-00 [ICM,7,C*];
                       A61K0038-08 [ICS,7]; A61P0019-02 [ICS,7]; A61P0019-00
                       [ICS,7,C*]; A61P0037-06 [ICS,7]; A61P0037-00 [ICS,7,C*]
                IPCR
                       A61K0038-00 [N,A]; A61K0038-00 [N,C*]; C07K0007-00
                       [I,C*]; C07K0007-06 [I,A]
JP 2006508901
                IPCI
                       C07K0007-06 [I,A]; C07K0007-00 [I,C*]; A61P0019-02
                       [I,A]; A61P0019-00 [I,C*]; A61P0029-00 [I,A];
                       A61K0038-00 [I,A]
                FTERM
                       4C084/AA02; 4C084/AA03; 4C084/AA07; 4C084/BA01;
                       4C084/BA08; 4C084/BA17; 4C084/CA59; 4C084/NA14;
```

4C084/ZB152; 4H045/AA10; 4H045/AA30; 4H045/BA15; 4H045/EA20; 4H045/FA20

- AB The invention provides the amino acid sequences of 7 non-T lymphocyte binding peptides derived from collagen type II, which contain the consensus sequence and may be recognized only by HLA-DRβ1 but not by T lymphocyte receptors. The non-T lymphocyte binding peptides bind to target consensus sequence QK/RRAA. The invention relates to uses of the non-T lymphocyte binding peptides for treating rheumatoid arthritis. The invention further relates to construction of rat model with CIA collagens induced arthritis and treating CIA with non-T lymphocyte binding peptides.
- ST non T lymphocyte binding peptide rheumatoid arthritis therapy; T cell activation HLA DR1 DR4 peptide rheumatoid arthritis
- IT Histocompatibility antigens
 - RL: BSU (Biological study, unclassified); BIOL (Biological study) (HLA-DR1, peptides binding to; non-T lymphocyte binding peptides derived from collagen type II and uses in treating rheumatoid arthritis)
- IT Histocompatibility antigens
 - RL: BSU (Biological study, unclassified); BIOL (Biological study) (HLA-DR4, peptides binding to; non-T lymphocyte binding peptides derived from collagen type II and uses in treating rheumatoid arthritis)
- IT Cell activation
 - (T cell, inhibition of; non-T lymphocyte binding peptides derived from collagen type II and uses in treating rheumatoid arthritis)
- IT T cell (lymphocyte)
 - (activation, inhibition of; non-T lymphocyte binding peptides derived from collagen type II and uses in treating rheumatoid arthritis)
- IT Disease models
 - (collagens induced arthritis; non-T lymphocyte binding peptides derived from collagen type II and uses in treating rheumatoid arthritis)
- IT Antirheumatic agents
 - Rheumatoid arthritis
 - (non-T lymphocyte binding peptides derived from collagen type II and
 uses in treating rheumatoid arthritis)
- IT Peptides, biological studies
 - RL: BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
 - (non-T lymphocyte binding peptides derived from collagen type II and uses in treating rheumatoid arthritis)
- IT Collagens, biological studies
 - RL: BSU (Biological study, unclassified); BIOL (Biological study) (type II; non-T lymphocyte binding peptides derived from collagen type II and uses in treating rheumatoid arthritis)
- IT 620973-81-1 620973-82-2 620973-83-3 620973-84-4
 - 620973-85-5 620973-86-6 620973-87-7
 - RL: BSU (Biological study, unclassified); PRP (Properties); THU
 - (Therapeutic use); BIOL (Biological study); USES (Uses)
 - (non-T lymphocyte binding peptide; non-T lymphocyte binding peptides
 derived from collagen type II and uses in treating rheumatoid
 arthritis)
- IT 620973-82-2
 - RL: BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses) (non-T lymphocyte binding peptide; non-T lymphocyte binding peptides derived from collagen type II and uses in treating rheumatoid
- arthritis)
 RN 620973-82-2 HCAPLUS
- CN L-Glutamic acid, L-phenylalanyl-L-lysylglycyl-L- α -glutamyl-L-glutaminyl-L-alanyl-L-prolyl-L-lysylglycyl- (9CI) (CA INDEX NAME)

Absolute stereochemistry.

11

HO₂C

PAGE 1-B

S

L7 ANSWER 3 OF 4 HCAPLUS COPYRIGHT 2006 ACS on STN

AN 2003:668434 HCAPLUS

DN 139:363392

ED Entered STN: 27 Aug 2003

TI Inhibition of T-cell activation with HLA-DR1/DR4 restricted non-T-cell stimulating peptides

AU Zhou, Qiang; Cheng, Yongjing; Lu, Houshan; Zhou, Weihong; Li, Zhanguo

CS People's Hospital, Arthritis Research Institute, Department of Rheumatology and Immunology (Q.Z., Y.C., H.L, Z.L.), Peking University Medical School, Beijing, Peop. Rep. China

SO Human Immunology (2003), 64(9), 857-865

CODEN: HUIMDQ; ISSN: 0198-8859

PB Elsevier Science Inc.

DT Journal

LA English

CC 15-8 (Immunochemistry)

AB It has been reported that collagen II (CII) derived peptide CII263-272

jan delaval - 26 june 2006

induced T-cell activation via its amino acids responsible for T-cell receptor (TCR) recognition. The impact of substitution of the TCR contacting amino acids of CII263-272 on T-cell activation was evaluated using a panel of altered CII263-272 peptides. Computer modeling revealed that the side chains of 263F and 266E in CII263-272 were coupled with amino acids on αl and βl chains of HLA-DR1 or -DR4, mainly via hydrogen bonds, whereas the side chains of 267Q and 270K protrude out of the cleft and might be recognized by TCR. Intracellular delivery of the altered peptides, and their binding to HLA-DR1 and -DR4 mols. on cell surface, were demonstrated by confocal microscopy and flow cytometry. results also revealed that the substitution of 267Q, 268G, 269P, and 270K individually or consecutively by alanine (A) or glycine (G) led to weak or non-T-cell responses. Furthermore, the altered peptides with 270K substitution (270A) or with consecutive substitution of 268G, 269P, and 270K (sub268-270) dramatically inhibited T-cell activation. It is suggested that the altered peptides derived from CII263-272 with substitution of amino acids responsible for TCR contact might be of inhibitory effect on T-cell responses.

ST T cell activation HLA DR1 DR4 peptide rheumatoid arthritis

IT Histocompatibility antigens

RL: BSU (Biological study, unclassified); BIOL (Biological study) (HLA-DR1; T-cell activation inhibition with HLA-DR1/DR4 restricted non-T-cell stimulating peptides derived from collagen type II)

IT Histocompatibility antigens

RL: BSU (Biological study, unclassified); BIOL (Biological study) (HLA-DR4; T-cell activation inhibition with HLA-DR1/DR4 restricted non-T-cell stimulating peptides derived from collagen type II)

IT Structure-activity relationship

(T cell-inhibiting; T-cell activation inhibition with HLA-DR1/DR4 restricted non-T-cell stimulating peptides derived from collagen type II)

IT Peptides, biological studies

TCR (T cell receptors)

RL: BSU (Biological study, unclassified); BIOL (Biological study) (T-cell activation inhibition with HLA-DR1/DR4 restricted non-T-cell stimulating peptides derived from collagen type II)

IT Human

Rheumatoid arthritis

(T-cell activation inhibition with HLA-DR1/DR4 restricted non-T-cell stimulating peptides derived from collagen type II in relation to rheumatoid arthritis therapy)

IT T cell (lymphocyte)

(activation; T-cell activation inhibition with HLA-DR1/DR4 restricted non-T-cell stimulating peptides derived from collagen type II)

IT Collagens, biological studies

RL: BSU (Biological study, unclassified); BIOL (Biological study) (type II; T-cell activation inhibition with HLA-DR1/DR4 restricted non-T-cell stimulating peptides derived from collagen type II)

IT 620973-80-0 620973-81-1 **620973-82-2** 620973-83-3 620973-84-4 620973-85-5 620973-86-6 620973-87-7

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)

(T-cell activation inhibition with HLA-DR1/DR4 restricted non-T-cell stimulating peptides derived from collagen type II)

RE.CNT 37 THERE ARE 37 CITED REFERENCES AVAILABLE FOR THIS RECORD RE

- (1) Aharoni, R; Eur J Immunol 1993, V23, P17 HCAPLUS
- (2) Andersson, E; Proc Natl Acad Sci USA 1998, V95, P7574 HCAPLUS
- (3) Deighton, C; Ann Rheum Dis 1993, V52, P638 MEDLINE
- (4) Dessen, A; Immunity 1997, V7, P473 HCAPLUS

(5) Diab, B; Immunogenetics 1999, V49, P36 HCAPLUS (6) Fremont, D; Science 1996, V272, P1001 HCAPLUS (7) Fridkis-Hareli, M; Cell Immunol 1995, V163, P229 HCAPLUS (8) Fridkis-Hareli, M; Hum Immunol 2000, V61, P640 HCAPLUS (9) Fridkis-Hareli, M; J Immunol 1998, V160, P4386 HCAPLUS (10) Fridkis-Hareli, M; Proc Natl Acad Sci USA 1994, V91, P4872 HCAPLUS (11) Fridkis-Hareli, M; Proc Natl Acad Sci USA 1998, V95, P12528 HCAPLUS (12) Fugger, L; Eur J Immunol 1996, V26, P928 HCAPLUS (13) Fugger, L; Proc Natl Acad Sci USA 1994, V91, P6151 HCAPLUS (14) Gao, X; Arthritis Rheum 1991, V34, P547 MEDLINE (15) Ghosh, P; Nature 1995, V378, P457 HCAPLUS (16) Goodford, P; J Med Chem 1985, V28, P849 HCAPLUS (17) Gregersen, P; Arthritis Rheum 1987, V30, P1205 HCAPLUS (18) Gregersen, P; Proc Natl Acad Sci USA 1986, V83, P2642 HCAPLUS (19) Hammer, J; J Exp Med 1995, V181, P1847 HCAPLUS (20) Jardetzky, T; Nature 1994, V368, P711 HCAPLUS (21) Kim, H; Arthritis Rheum 1999, V42, P2085 HCAPLUS (22) Morris, G; AutoDock 1999, V3.0 (23) Morris, G; J Comp Chem 1998, V19, P1639 HCAPLUS (24) Myers, L; J Immunol 1998, V161, P3589 HCAPLUS (25) Nepom, G; Arthritis Rheum 1989, V32, P15 MEDLINE (26) Ohta, N; Hum Immunol 1982, V5, P23 (27) Rammensee, H; Immunogenetics 1995, V41, P178 HCAPLUS (28) Rosloniec, E; Cell Immunol 1996, V172, P21 HCAPLUS (29) Rosloniec, E; J Exp Med 1997, V185, P113 (30) Rosloniec, E; J Immunol 2002, V168, P253 HCAPLUS (31) Sanchez, B; Tissue Antigens 1990, V36, P174 MEDLINE (32) Sharp, K; Science 1987, V236, P1460 HCAPLUS (33) Stern, L; Nature 1994, V368, P215 HCAPLUS (34) Teitelbaum, D; J Neuroimmunol 1996, V64, P209 HCAPLUS (35) Teitelbaum, D; Proc Natl Acad Sci USA 1992, V89, P137 HCAPLUS (36) Willkens, R; Arthritis Rheum 1991, V34, P43 MEDLINE (37) Zhou, Q; Chin J Rheumatol 2002, V6, P397 ΙT 620973-82-2 RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study) (T-cell activation inhibition with HLA-DR1/DR4 restricted non-T-cell stimulating peptides derived from collagen type II) RN 620973-82-2 HCAPLUS CN L-Glutamic acid, L-phenylalanyl-L-lysylglycyl-L-α-glutamyl-L-

glutaminyl-L-alanyl-L-prolyl-L-lysylglycyl- (9CI) (CA INDEX NAME)

Absolute stereochemistry.

PAGE 1-A

Ph
$$H_2N$$
 H_2N H_2N H_3N H_4N H_5 H_5 H_5 H_5 H_7 H_8 $H_$

PAGE 1-B

$$-\frac{H}{N}$$
 $\frac{CO_2H}{S}$ CO_2H CO_2H O

L7 ANSWER 4 OF 4 HCAPLUS COPYRIGHT 2006 ACS on STN

AN 1998:414290 HCAPLUS

DN 129:160544

ED Entered STN: 08 Jul 1998

TI Definition of MHC and T cell receptor contacts in the HLA-DR4-restricted immunodominant epitope in type II collagen and characterization of collagen-induced arthritis in HLA-DR4 and human CD4 transgenic mice

AU Andersson, Ellen Christina; Hansen, Bjarke Endel; Jacobsen, Helle; Madsen, Lars S.; Andersen, Claus B.; Engberg, Jan; Rothbard, Jonathan B.; Sonderstrup McDevitt, Grete; Malmstrom, Vivianne; Holmdahl, Rikard; Svejgaard, Arne; Fugger, Lars

CS Department of Clinical Immunology, Rigshospitalet, Copenhagen, 2200 N, Den.

SO Proceedings of the National Academy of Sciences of the United States of America (1998), 95(13), 7574-7579
CODEN: PNASA6; ISSN: 0027-8424

PB National Academy of Sciences

DT Journal

LA English

CC 15-8 (Immunochemistry)

```
AB
     Rheumatoid arthritis (RA) is an autoimmune disease associated with the
     HLA-DR4 and -DR1 alleles. The target autoantigen(s) in RA is unknown, but
     type II collagen (CII) is a candidate, and the DR4- and DR1- restricted
     immunodominant T cell epitope in this protein corresponds to amino acids
     261-273 (CII 261-273). The authors have defined MHC and T cell receptor
     contacts in CII 261-273 and provide strong evidence that this peptide
     corresponds to the peptide binding specificity previously found for
     RA-associated DR mols. Moreover, they demonstrate that HLA-DR4 and human CD4
     transgenic mice homozygous for the I-Abβ0 mutation are highly
     susceptible to collagen-induced arthritis and describe the clin. course
     and histopathol. changes in the affected joints.
ST
    MHC TCR contact epitope II collagen
IT
    Histocompatibility antigens
    RL: BOC (Biological occurrence); BSU (Biological study, unclassified);
    BIOL (Biological study); OCCU (Occurrence)
        (HLA-DR1; MHC and TCR receptor contacts in HLA-DR4-restricted
        immunodominant epitope in type II collagen and characterization of
        collagen-induced arthritis in HLA-DR4 and human CD4 transgenic mice)
IT
    Histocompatibility antigens
    RL: BOC (Biological occurrence); BSU (Biological study, unclassified);
    BIOL (Biological study); OCCU (Occurrence)
        (HLA-DR4; MHC and TCR receptor contacts in HLA-DR4-restricted
        immunodominant epitope in type II collagen and characterization of
        collagen-induced arthritis in HLA-DR4 and human CD4 transgenic mice)
IT
     Epitopes
    Rheumatoid arthritis
     T cell (lymphocyte)
        (MHC and TCR receptor contacts in HLA-DR4-restricted immunodominant
        epitope in type II collagen and characterization of collagen-induced
        arthritis in HLA-DR4 and human CD4 transgenic mice)
TΤ
    CD4 (antigen)
    TCR (T cell receptors)
    RL: BOC (Biological occurrence); BSU (Biological study, unclassified);
    BIOL (Biological study); OCCU (Occurrence)
        (MHC and TCR receptor contacts in HLA-DR4-restricted immunodominant
        epitope in type II collagen and characterization of collagen-induced
        arthritis in HLA-DR4 and human CD4 transgenic mice)
IT
    Arthritis
    Arthritis
        (autoimmune, collagen-induced; MHC and TCR receptor contacts in
        HLA-DR4-restricted immunodominant epitope in type II collagen and
        characterization of collagen-induced arthritis in HLA-DR4 and human CD4
        transgenic mice)
TΤ
    Collagens, biological studies
    RL: ADV (Adverse effect, including toxicity); BIOL (Biological study)
        (type II; MHC and TCR receptor contacts in HLA-DR4-restricted
        immunodominant epitope in type II collagen and characterization of
        collagen-induced arthritis in HLA-DR4 and human CD4 transgenic mice)
TΤ
    175800-89-2
                   211099-06-8
                                 211099-07-9
                                               211099-08-0
                                                             211099-09-1
    211099-10-4
                   211099-11-5 211099-13-7
                                             211099-14-8
    211099-15-9
                   211099-16-0
                                 211099-17-1
                                               211099-18-2
                                                             211099-19-3
    211099-20-6
                   211099-21-7
                                 211099-22-8
                                               211099-23-9
                                                             211099-24-0
    RL: PRP (Properties)
        (MHC and TCR receptor contacts in HLA-DR4-restricted immunodominant
        epitope in type II collagen and characterization of collagen-induced
        arthritis in HLA-DR4 and human CD4 transgenic mice)
RE.CNT
       37
             THERE ARE 37 CITED REFERENCES AVAILABLE FOR THIS RECORD
RF.
(1) Casanova, J; J Exp Med 1991, V174, P1371 HCAPLUS
```

(2) Cathcart, E; Lab Invest 1986, V54, P26 MEDLINE

(3) Clague, R; Arthritis Rheum 1984, V27, P1370 MEDLINE (4) Cook, A; Arthritis Rheum 1996, V39, P1720 MEDLINE (5) Cope, A; Functional and Medical Implication 1997, P634 HCAPLUS (6) Courtenay, J; Nature 1980, V283, P666 HCAPLUS (7) Dessen, A; Immunity 1997, V7, P473 HCAPLUS (8) Feldmann, M; Cell 1996, V85, P307 HCAPLUS (9) Fugger, L; Eur J Immunol 1996, V26, P928 HCAPLUS (10) Fugger, L; Proc Natl Acad Sci USA 1994, V91, P6151 HCAPLUS (11) Fugger, L; Tissue Antigens 1997, V50, P494 HCAPLUS (12) Garboczi, D; Nature 1996, V384, P134 HCAPLUS (13) Gregersen, P; Arthritis Rheum 1987, V30, P1205 HCAPLUS (14) Grusby, M; No publication given 1991, V253, P1417 HCAPLUS (15) Hammer, J; J Exp Med 1995, V181, P1847 HCAPLUS (16) Hansen, B; Tissue Antigens 1998, V51, P119 HCAPLUS (17) Holmdahl, R; Human Genome Methods 1998, P215 HCAPLUS (18) Holmdahl, R; Immunol Rev 1990, V118, P193 HCAPLUS (19) Holmdahl, R; Lab Invest 1988, V58, P53 MEDLINE (20) Jasin, H; Arthritis Rheum 1985, V28, P241 MEDLINE (21) Londei, M; Proc Natl Acad Sci USA 1988, V86, P636 (22) Marshall, K; J Immunol 1995, V154, P5927 HCAPLUS (23) Michaelsson, E; J Exp Med 1994, V180, P745 HCAPLUS (24) Nabozny, G; J Exp Med 1996, V183, P27 HCAPLUS (25) Osman, G; J Exp Med 1993, V177, P387 HCAPLUS (26) Patel, S; Proc Natl Acad Sci USA 1997, V94, P8082 HCAPLUS (27) Rammensee, H; Immunogenetics 1995, V41, P178 HCAPLUS (28) Rock, E; J Exp Med 1994, V179, P323 HCAPLUS (29) Ronnelid, J; Arthritis Rheum 1994, V37, P1023 MEDLINE (30) Rosloniec, E; J Exp Med 1997, V185, P1113 HCAPLUS (31) Rowley, M; Ann Rheum Dis 1990, V49, P578 MEDLINE (32) Schmidt, D; J Exp Med 1997, V186, P1059 HCAPLUS (33) Stern, L; Nature 1994, V368, P215 HCAPLUS (34) Tarkowski, A; Arthritis Rheum 1989, V32, P1087 MEDLINE (35) Trentham, D; J Exp Med 1977, V146, P857 MEDLINE (36) Zanelli, E; Immunol Today 1995, V16, P274 HCAPLUS (37) Zanelli, E; Proc Natl Acad Sci USA 1996, V93, P1814 HCAPLUS IΤ 211099-13-7 RL: PRP (Properties) (MHC and TCR receptor contacts in HLA-DR4-restricted immunodominant epitope in type II collagen and characterization of collagen-induced

arthritis in HLA-DR4 and human CD4 transgenic mice)

L-Proline, L-alanylglycyl-L-phenylalanyl-L-lysylglycyl-L- α -glutamyl-L-glutaminyl-L-alanyl-L-prolyl-L-lysylglycyl-L- α -glutamyl- (9CI)

(CA INDEX NAME)

Absolute stereochemistry.

211099-13-7 HCAPLUS

RN

CN

PAGE 1-A

PAGE 2-A

Ph
$$\stackrel{S}{\longrightarrow} \stackrel{H}{\longrightarrow} \stackrel{N}{\longrightarrow} \stackrel$$

```
collagen 13, nonfi
hypothetical prote
collagen alpha 1(V
collagen alpha 1(V
collagen alpha 1(V
collagen alpha 1(V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     collagen alpha 1(I
collagen alpha 1(I
collagen alpha 1(I
collagen alpha 1/(
collagen alpha 2(V
procollagen type V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical prote
hypothetical prote
collagen alpha 1(V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALG3 protein - yea
valine-tRNA ligase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       molybdenum cofacto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    surfacta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          collagen short cha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       surfactant protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            transforming growt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein - equi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             collagen alpha 1 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene Tl protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                            (without alignments)
24.671 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pulmonary
                                                                              June 23, 2006, 21:08:50 ; Search time 39 Seconds
GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                          cal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                  283416 seqs, 96216763 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
                                                                                                                                                                                                                                                                                                                             st-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                    protein - protein search, using sw model
                                                                                                                                                                                         BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A40333
CGHU2V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                841182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B98047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5435
                                                                                                                                                                                                                                                                                        nimum DB seq length: 0 cimum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query
Match Length DB
                                                                                                                                   US-10-519-524-2
54
                                                                                                                                                              1 FKGEQAPKGE 10
                                                                                                                                                                                                                                                                                                                                                                                                  piri:
piri:
piri:
pir4:
                                                                                                                                                                                                                                                                                                                                                                                      PIR 80:*
                                                                                                                                                                                         oring table:
                                                                                                                                                   rfect score:
                                                                                                                                                                 mence:
                                                                                                                                                                                                                                   arched:
                                                                                                                                                                                                                                                                                                                                                                                        cabase
                                                                                  no c
```

collagen alpha 1(X	nonhistone chromos	hypothetical prote	collagen alpha 2(V	probable tail-host	collagen alpha 1(I	collagen alpha 6(I	collagen alpha 1(V	collagen alpha 1(V	hypothetical prote	conserved hypothet	hypothetical prote				
A53317	NSBOH7	S11349	833866	803700	801946	T29773	A57131	T13334	B34493	CGHU6B	CGHUIV	S18803	T13518	AB3070	T22637
7	-	~	N	7	~	~	N	~	N	-	~	N	N	7	0
1388	89	89	83	90	8	396	635	843	920	1691	1838	1843	181	261	287
68.5	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	64.8	64.8	64.8
37	36	36	36	36	36	36	36	36	36	36	36	36	35	35	35
30	31	32	33	34	35	36	37	38	39	40	41	42	43	4	45

ALIGNMENTS

```
A;Rolecule type: protein
A;Rolecule type: protein
A;Rosaleus: 1-15 -MILD-
A;Rosaleus: 1-15 -MILD-
A;Crosalereferences: UNIPROT:P02459; UNIPARC:UPI0000173B79
A;Roserimental source: cartilage
A;Rober residues positioned by comparison with human alpha 1(II) chain
A;Rober: w.T.; Milor, E.J.; Finch Jr., J.B.
Biochemistry 15, 3000-3006, 1976
A;Tille: The covalant structure of cartilage collagen. Amino acid sequence of the NH-2-tt
A;Reference number: A90396; MUD:76253504; PMID:782511
A;Reference number: A90396; MUD:76253504; PMID:782511
A;Robersion: A90396
                                                                                                                                                                                                                                                                                                                                                                              A; Cross-references: UNIPROT: Q63123; UNIPARC: UPI000014D4E6; EMBL: X79816; NID: 9531375; PIDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           bromide peptides from the alphal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; uene: 11
C; Superfamily: fibrillar collagen carboxyl-terminal homology; von Willebrand factor type
                                               C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 31-Dec-2004 C;Accession: 160384 Rsimichaelsson, E.; Malmstrom, V.; Reis, S.; Engstrom, A.; Burkhardt, H.; Holmdahl, R. Exp. Med. 180, 745-749, 1994 A;Title: T cell recognition of carbohydrates on type II collagen. A;Reference number: 160384; MUID:94321934; PMID:8046350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          collagen alpha 1(II) chain precursor - bovine (tentative sequence) (fragments)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Bos primigenius taurus (cattle).
C;Species: Bos primigenius taurus (cattle).
C;Date: 24-Apr-1984 #sequence revision 17-May-1996 #text_change 09-Jul-2004
C;Accession: A90369; A90396; Ā92210; S03940; A90189; A05039; A02859
R;Miller, E.J.; Lunde, L.G.
Biochemistry 12, 3153-3159, 1973
Biochemistry 12, 3153-3159, 1973
A;Title: Isolation and characterization of the cyanogen bromide peptides fxt
A;Reference number: A90369; MUID:73258693; PMID:4732855
A;Contents: composition of CNBr1 and CNBr4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 50; DB 2; Length 53;
Pred, No. 0.014;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                     A;Status: preliminary; translated from GB/EMBL/DDBJ
                           C;Species: Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92.6%;

    rat (fragment)

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 90..
Best Society 90..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FKGEQAPKGE 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PKGEOGPKGE 35
                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-53 <RES>
                                                                                                                                                                                                                                                                 A; Accession: I60384
gene Tl protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56
                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene: Tl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
```

A;Molecule type: protein

```
C,Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: B4033
R;Su, M.W.; Suzuki, H.R.; Bieker, J.J.; Solursh, M.; Ramirez, F.
A;Ttele: Expression of two nonallelic type II procollagen genes during Xenopus laevis emt
A;Accession: B4033
A;Accession: B40333
A;Scession: B40333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NyAlternate names: procollagen alpha i(II) chain
NyContains: achouf-ocalcin; collagen alpha 1(II) chain precursor splice form 1; collagen & NyContains: chonfocalcin; collagen alpha 1(II) chain precursor splice form 1; collagen & C.Species: Homo sapiens (man)
C.Date: 28-May-1986 #sequence revision 01-Sep-1995 #text change 31-Dec-2004
C.Accession: ASB13; S06715; S24770; A24828; S06496; A35428; A30147; A33116, S64674; S63: C.Secssion: ASB13; 137252; I37253; I37254; I55338; I55935; I61910
R.Ryan, M.C.; Sleraski, M.; Sandell, L.J.
Genomics & 41-48, 1990
A;Fille: The human type II procollagen gene: identification of an additional protein-codi A;Reference number: A38513; MUID:91184811; PMID:2081599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Molecule type: mRNA,
MResidues: 1-1486 <SUA.>
A,Residues: 1-1486 <SUA.>
A,Residues: 1-1486 <SUA.>
A,Residues: 1-1486 <SUA.
A,Cross-references: UNIRROT:091718; UNIPROT:091717; UNIPARC:UPI0000173B50; GB:M63595
C,Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology;
C,Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology of C,Reywords collagen factor type C repeat homology <VWC>
F;37-96/Domain: von Willebrand factor type C repeat homology <VWC>
F;1258-1486/Domain: fibrillar collagen carboxyl-terminal homology <FCC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R.Su. M.W.; Lee, B.; Ramirez, F.; Machado, M.; Horton, W.
Nucleic Acids Res. 17, 9473, 1989
A;Title: Nucleotide sequence of the full length cDNA encoding for human type II procollag
A;Reference number: 806715; WUID:90067946; PMID:2587267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Molecule type: mRNA
A,Residues: 1-28, 'R',99-1487 <SU2>
A,Cross-references: UNIPARC:UDI0000126D15; EMBL:X16468; NID:g29515; PIDN:CAA34488.1; PID:
A,Note: alternative splice form 1
R;Vikkula, M; Meteaeranta, M.; Syvaenen, A.C.; Ala-Kokko, L.; Vuorio, E.; Peltonen, L.
Biochem. J. 285, 287-294, 1992
A;Title: Structural analysis of the regulatory elements of the type-II procollagen gene.
A,Molecule type: mRNA
A,Residues: 1-1418 cRIC-
A;Cross-references: UNIPROT:Q28396; UNIPARC:UPI000008834A; EMBL:U62528; PIDN:AAB05773.1
C;Superfamily: collagen alpha 1(1) chain; fibrillar collagen carboxyl-terminal homology;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: UNIPROT:P02458; UNIPROT:Q14042; UNIPROT:Q16672; UNIPROT:Q12985; UNIPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 collagen alpha 1(II) chain precursor - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gape
                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 50; DB 1; Length 1486;
Pred. No. 0.41;
0; Mismatches 1; Indels
                                                                                                                                                                                                        DB 2; Length 1418;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          collagen alpha 1(II) chain precursor [validated] - human
                                                                                                                                                                                                                                          0.39;
                                                                                                                                                                                                   Score 50; DB
Pred. No. 0.39
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92.6%;
                                                                                                                                                                                               Query Match 92.6%;
Best Local Similarity 90.0%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 92.6
Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                  403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      465 FKGEQGPKGE 474
                                                                                                                                                                                                                                                                                                                                                                 1 FKGEQAPKGE 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 FKGEQAPKGE 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                  394 PKGEOGPKGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A, Accession: A38513
A, Molecule type: DNA
A, Residues: 1-103 <RYA>
                                                                                                                                                                                                                                                                                                                                                                     ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                    Molecule type: protein
Residues: 139-176, Z', 180-184, PA', 187-190, 'AS', 193-194,'T', 196-198 <BU2>
Cross-references: UNIPARC:UPI0000173B7B
Experimental source: cartilage
Note: a minor, probably nonallelic, alpha 1(II) component has 143-Ala, 164-Leu, and pc Seyer. J.M.; Hasty, K.A.; Kang, A.H.
Ir. J. Biochem. 181, 159-173, 1889
Title: Covalent structure of collagen. Amino acid sequence of an arthritogenic cyanoge Reference number: S03940; MUID:89231683; PMID:2714276
                                                                        Experimental source: cartilage
Note: order of CNBr peptides determined
Butler, W.T., Finch Jr., J.E.; Miller, E.J.
Biol. Chem. 252, 639-641
Title: The covalent structure of cartilage collagen. Evidence for sequence heterogenei
Reference number: A92210; MUID:77093864; PMID:833147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Experimental source: cartilage

Comment: Prolines in the third position of the tripeptide repeating unit (G-X-Y) are h

Comment: Prolines in the third position of the tripeptide repeating unit (G-X-Y) are h

COMMENT: Type II collagen molecules are trimers of identical alpha 1(II) chains, genet

COMMENT: Type II collagen molecules are trimers of identical alpha 1(II) chains, genet

Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology;

Keywords: cartilage; coiled coil; extracellular matrix; glycoprotein; hydroxylysine; type-673/Domain: carboxyl-terminal propeptide (fragment) #status predicted cCTP-

499-673/Domain: fibrillar collagen carboxyl-terminal homology (fragment) *FCC>

9,102,114,123,189,423,435/Binding site: Shydroxylysine (Lys) #status experimental

9,102,114,123,189, 423,435/Binding site: Sarbohydrate (Lys) (covalent) #status experime

574/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Butler, W.T.; Miller, E.J.; Finch Jr., J.B.; Inagami, T.
ochem. Biophys. Res. Commun. 57, 190-195, 1974
Title: Homologous regions of collagen alphal (I) and alphal(II) chains: apparent clust
Reference number: A90189; MUID:74163168; PWILD:4857180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Residues: 493-673 <SAN>
Cross-references: UNIPARC:UP1000016C2E1; GB:X02420; NID:g265; PIDN:CAA26269.1; PID:g26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Richardson, D.W.; Dodge, G.R.
bmitted to the EMBL Data Library, June 1996
Description: Cloning of equine type II collagen and modulation of its expression in
Reference number: 222977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Experimental source: cartilage
Note: the first 75 residues of CNBrB, which follows CNBrll
Sangiorgl, P.O.; Benson-Chanda, V.; de Wet, W.J.; Sobel, M.E.; Ramirez, F.
cleic Acids Res. 13, 2815-2826, 1985
Reference number: A05039; MUID:85215651; PMID:2582365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           liagen alpha 1(II) chain precursor [imported] - horse
Alternate names: type II collagen
Species: Equus caballus (domestic horse)
Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 50; DB 1; Length 673; Pred. No. 0.18; 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Molecule type: protein
Residues: 139-417 <SEY>
Cross-references: UNIPARC:UP10000173B7C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Molecule type: protein
Residues: 418-492 <BU3>
Cross-references: UNIPARC:UP10000173B7D
                                      Cross-references: UNIPARC:UPI0000173B7A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           278 FKGEQGPKGE 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 FKGEQAPKGE 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Accession: S03940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Accession: T45467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Accession: A90189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Accession: A05039
```

```
COZA1
                                                                                                                                                                                                                                                                                                                                            homo sapien
homo sapien
m bone marr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tetraodon n
tetraodon n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            xenopus lae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          xenopus lae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           xenopus tro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            homo sapien
equus cabal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        canis famil
mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mus musculu
mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            xenopus lae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          brachydanio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             brachydanio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gallus gall
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              сулорв ругі
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rattus nor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gallue gall
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                           (without alignments)
31.251 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mus :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0071227

00408

004079

004079

0070717

0070717

007077

007077

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707

00707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q53wr4
Q3u962
                                                                                             ; Search time 296 Seconds
GenCore version 5.1.9
(c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                     tal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                          2849598 segs, 925015592 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOUSE
MOUSE
MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHICK
HUMAN
HORSE
CYNPY
RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          XENLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        XENLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TETNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q8AW11_BRARE
Q96OB3_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q53WR4 HUMAN
Q3U962 MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          XENLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         XENTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TETNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CO2A1 BOVIN
Q7T2Z7 CHIC
                                                                                                                                                                                                                                                                                                                                                                                         st-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                             - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          091718
06P4Z2
                                                                                            June 23, 2006, 21:05:20
                                                                                                                                                                                                                                           Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04SK66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q4RX03
                                                                                                                                                                                                                                                                                                                                                                                                                                                          UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*
                                                                                                                                                                                                                                                                                                                                         nimum DB seq length: 0 ximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query
Match Length DB
                                                                                                                                                           US-10-519-524-2
54
                                                                                                                                                                                        1 PKGEQAPKGE 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1442
1459
1459
1487
1491
             Copyright
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1492
                                                                                                                                                                                                                          BLOSUM62
                                                                                                                                                                                                                          oring table:
                                                                                                                                                                              rfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score
                                                                                                                                                                                             quence:
                                                                                                                                                                                                                                                                        arched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           tabase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
```

Q3uhk7 mus musculu Q3v1j6 mus musculu Q61431 mus musculu Q51ip2 mus musculu Q55ip2 sus scrofa Q59gr4 homo sapien Q6vz1 homo sapien Q6vz1 homo sapien Q6vz3 mus musculu Q7z41 homo sapien Q7z41 homo sapien Q9cuc3 mus musculu Q8r37 mus musculu Q8r37 mus musculu Q8r37 homo sapien Q8hzz2 mus musculu Q8hzz7 homo sapien
Q3UHK7 MOUSE Q3V1J6_MOUSE Q61431 MOUSE Q7TMS0_MOUSE Q59IR2_HUMAN Q6UXZ1_HUMAN Q9D4G8_MOUSE Q87330_MOUSE Q8RZZZ_MOUSE Q8RZZZ_MOUSE Q8RZZZ_MOUSE Q8RZZZ_MOUSE Q8RZZZ_MOUSE
000000000000000
1497 1497 1497 1497 1502 280 280 283 357 375 400 491
811.5 811.5 811.5 811.5 7.7 7.7 7.7 7.7 7.7 7.7 7.7 7.7 7.7 7
ቀ ቁ ቁ ቁ ቁ ቁ ቁ ቁ ቁ ቁ ቁ ቁ ቁ ቁ ቁ ቁ ቁ ቁ ቁ ቁ
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~

# ALIGNMENTS

```
TISSUE=Cartilage;
MEDLINE=89231683; PubMed=2714276;
Seyer J.M., Hasty K.A., Kang A.H.;
"Covalent structure of collagen. Amino acid sequence of an arthritogenic cyanogen bromide peptide from type II collagen of bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUB=Cartilage,
MEDLINE=76253504; PubMed=782511;
Butler W.T., Miller B.J., Finch J.E. Jr.,
"The covalent structure of cartilage collagen. Amino acid sequence of
the NH2-terminal helical portion of the alpha 1 (II) chain.";
Biochemistry 15:3000-3006(1976).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROTEIN SEQUENCE OF 418-492, HYDROXYLATION SITES LYS-9; LYS-102;
LYS-114; LYS-123; LYS-189; LYS-423 AND LYS-435, AND
CARBOHYDRATE-LINKAGE SITES LYS-9; LYS-102; LYS-114; LYS-123; LYS-189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Cartilage;
MEDLINE=77093864; PubMed=833147;
Butler W.T., Finch J.E. Jr., Miller E.J.;
"The covalent structure of cartilage collagen. Evidence for sequence hererogeneity of bovine alphal(II) chains.";
J. Biol. Chem. 252:639-643(1977).
                                                                                                                                                                                                                                                                  Bos taurus (Bovine).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Bammalia, Eutheria, Laurasiatheria, Cetartiodactyla, Ruminantia,
Pecora, Bovidae, Bovinae, Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Cartilage;
MEDLINE=73258693; PubMed=4732855;
Miller E.J., Lunde L.G.;
Misolation and characterization of the cyanogen bromide peptides the alpha 1(II) chain of bovine and human cartilage collagen.";
Biochemistry 12:3153-3159(1973).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROTEIN SEQUENCE OF 139-198, AND VARIANTS ALA-143 AND LEU-164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LYS-423 AND LYS-435.
MEDLINE-74163168; PubMed=4857180;
Butler W.T., Miller B.J., Finch J.E. Jr., Inagami T.;
                         CO2A1 BOVIN STANDARD; PRT; 747 AA. P02459; Q28070; Q9XT24; 21-UUJ-1986, integrated into UniProtKB/Swiss-Prot. 30-MAY-2000, sequence version 3. O7-FEB-2006, entry version 63. Collagen alpha-1(II) chain precursor (Fragments). Name=COL2A1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eur. J. Biochem. 181:159-173(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROTEIN SEQUENCE OF 16-177.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROTEIN SEQUENCE OF 139-417.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROTEIN SEQUENCE OF 1-15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cartilage
BOVIN
```

N

```
CARBOHYD
CARBOHYD
CARBOHYD
MOD_RES
MOD_RES
MOD_RES
CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                              CARBOHYD
VARIANT
                                                                                                                                                                                                                                                                                                                                                             CONFLICT
CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHICK
                                                                                                                                                                                                                                                                                                                                     VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07T2Z7
  ଚ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; ALS9519; AAD42347.1; -; mRNA.

EMBL; A20320; CAAZ6269.1; -; mRNA.

PIR; A90369; CGBOCC.

PIR; A90369; CGBOCC.

InterPro; IPR008161; Clg helix.

InterPro; IPR008161; Clg helix.

InterPro; IPR008161; VWF_C.

Pfam; PP01391; Collagen.

Probom; PD002070; Flb collagen.

Probom; PD002070; Flb collagen.

PROSITE; PS01208; VWFC_1; 1.

PROSITE; PS01208; VWFC_1; 1.

PROSITE; PS01208; VWFC_1; 1.

PROPEP <567 747 C-terminal propeptide.

PROPEP <567 747 C-terminal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE (MRNA) OF 567-747.

NUCLEOTIDE SEQUENCE (MRNA) OF 567-747.

MEDLINE-8521561; PubMed=2582364.

Sangiorgi F.O., Benson-Chanda V., de Wet W.J., Sobel M.E., Ramirez F.; analysis of CDNA and genomic clones coding for the pro alpha 1 chain of calf type II collagen.";

Nucleic Acids Res. 13:2815-2826(1985).

It is essential for the normal embryonic development of the selecton, for linear growth and for the ability of cartilage to resist compressive forces.

SUBUNIT: Homorrimers of alpha 1(II) chains.

SUBUNIT: Homorrimers of alpha 1(II) chains.

SUBUNIT: Hydroxylation on Pro-9 is involved in cross-linking.

Chains. Hydroxylation on Pro-9 is involved in cross-linking.

Chains. Hydroxylation on Pro-9 is involved in cross-linking.

Hydroxylation of post-translationally added hydroxyl groups.

SIMILARITY: Belongs to the fibrillar collagen family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WÜCLEOTIDE SEQUENCE [WRNA] OF 417-566.

TISSUE=Cartilage;
MEDLINE=99440731; PubMed=10479530; DOI=10.1006/Clim.1999.4755;
MEDLINE=99440731; PubMed=10479530; DOI=10.1006/Clim.1999.4755;
Tang B., Chiang T.M., Brand D.D., Gumanovekaya M.L., Stuart J.M.,
Kang A.H., Myers L.K.;
"Molecular definition and characterization of recombinant bovine CB8
and CB10: 1mmunogenicity and arthritogenicity.";
"Homologous regions of collagen alpha1(I) and alpha1(II) chains: apparent clustering of variable and invariant amino acid residues."; Biochem. Biophys. Res. Commun. 57:190-195(1974).
                                                                                                                                                                                                                                                                        MEDIJURE-Cartillage.
MEDIJURE-Cartillage.
MEDIJURE-S4194070; PubMed=7511638;
MEDIJURE-94194070; PubMed=7511638;
MEDIJURE-94194070; PubMed=7511638;
METANG DA.H., Rosloniec B.F.;
"Characterization of the T cell determinants in the induction of autodimmune arthritis by bovine alpha 1(II)-CB11 in H-2q mice.";
J. Immunol. 152:3088-3097(1994).
                                                                                                                                       Brand D.D., Myers L.K., Terato K., Whittington K.B., Stuart J.M., Kang A.H., Rosloniec B.F.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5-hydroxylysine.
5-hydroxylysine.
5-hydroxylysine.
                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE [MRNA] OF 180-272.
                                                                                                            NUCLEOTIDE SEQUENCE [MRNA] OF 138-417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; L28918; AAA30436.2; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOD_RES
MOD_RES
MOD_RES
MOD_RES
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Copyrighted by the Uniprot Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xi C., Liu N., Liang F., Guo S., Sun Y., Yang F., Xi Y.; "Molecular cloning, characterization and localization of chicken type II procollagen gene."; Gene 366:67-76 (2006).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .gallus gallus (Chicken).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Calxia X., Yongzhi X., Siqi G., Yuying S.; "Gallus gallus alpha 1 type IIA collagen precursor (COL2A1)."; Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92.6%; Score 50; DB 1; Length 747; 90.0%; Pred. No. 2.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                   T -> Q (in Ref. 4).

S -> A (in Ref. 4).

P -> A (in Ref. 4).

P -> A (in Ref. 4).

Q -> T (in Ref. 4).

T -> S (in Ref. 4).

T -> S (in Ref. 4).

A -> T (in Ref. 6).

B -> S (in Ref. 6).

P -> S (in Ref. 6).

P -> A (in Ref. 6).

SPGAN -> PSGLA (in Ref. 6).

SPGEA -> ANGDP (in Ref. 6).
                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71330 MW; DOFCID7CDICAF77C CRC64;
                                                                                                                                                                                        AP -> PA (in Ref. 3).
EA -> AS (in Ref. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                      A -> P (in Ref. 6)
K -> R (in Ref. 6)
G -> P (in Ref. 5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-0CT-2003, integrated into UniProtKB/TrEMBL. 01-0CT-2003, sequence version 1. 07-MRZ-2006, entry version 12. Alpha 1 type II procollagen (Fragment). Name=COL2A1;
5-hydroxylysine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QT1227_CHICK PRELIMINARY; PRT; 1269 AA.
Q712277;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0, Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  278 FKGEQGPKGE 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 FKGEQAPKGE 10
                            NUCLEOTIDE SEQUENCE.
PubMed=16297573;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    566
747 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                           3359
3359
4359
4359
4359
4359
```

н

c

```
Immunomod
Human col
Human col
Peptide 2
Human col
Human col
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bovine ty
Type II c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human col
Immunomod
Immunomod
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Amino aci
Collagen
Bovine ty
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human col
Human col
Human col
Rheumatoi
Rheumatoi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gene 33 h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Collagen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                       June 23, 2006, 21:04:55; Search time 200 Seconds (without alignments) 22.861 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Aay82065
Aab84108
Aay82066
Aaw03107
Adc21570
Adc21570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Adc21600 Adf24(19 Adf14(19 Adf14(19 Adb9607) Adb96073 Adb92079 Adb96095 Adb66095 Adb66095 Adb66095 Adc21602 Adc21602 Adc21602 Adc21603 Adc21603 Adc21603 Adc21603 Adc21603 Adc21603 Adc21605 Adc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Aaw03105
GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                             tal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                              2589679 segs, 457216429 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        st-processing: Minimum Match 0*
Maximum Match 100*
Listing first 45 summaries
                                                                                        - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY82065
AAB84108
AAY82066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW03107
ADC21570
ADC21549
ADC21600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADF14619
AAB96873
AAB96873
AAB84091
AAB84093
AAB84094
AAB84095
AAB84095
AAB84095
AAB84095
AAB84095
AAB84095
AAB84095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADC21585
ADC21605
ADC21586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW03105
                                                                                                                                                                                                                                                                                                                                    Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              geneseqp2002s:*
geneseqp2003as:*
geneseqp2003bs:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           geneseqp1990s:*
geneseqp2000s:*
geneseqp2001s:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              geneseqp2006s:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        geneseqp1980s:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  geneseqp20048:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  geneseqp2005s:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nimum DB seq length: 0 ximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query
Match Length DB
                                                                                                                                                                                                                         US-10-519-524-2
54
                                                                                                                                                                                                                                                                     1 PKGEQAPKGE 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Geneseq 8:*
                                                                                                                                                                                                                                                                                                                 BLOSUM62
                                                                                                                                                                                                                                                                                                                 oring table:
                                                                                                                                                                                                                                                rfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ••
                                                                                                                                                                                                                                                                          quence:
                                                                                                                                                                                                                                                                                                                                                                                   arched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tabase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bult
No.
```

		Aab12273 Peptide u	Adr31655 Latent tr	Aau02072 Synthetic		Aab35625 CB11 pept	Aau02079 Synthetic	Aau02076 Synthetic			_		_		_	-	Aab35624 Human typ		Abb80735 Collagen		Abb09627 Amino aci	
ADC21606	AAR79479	AAB12273	ADR31655 .	AAU02072	AAU02078	AAB35625	AAU02079	AAU02076	AAU02077	ADC21544	AED95251	AED95261	ABM83560	AAR59751	AAR71703	AAY96124	AAB35624	AAE16477	ABB80735	ABG93927	ABB09627	
7	N	ო	æ	4	4	4	4	4	4	7	σ	σ	ω	~	~	٣	4	'n	Ŋ	Ŋ	Ŋ	
48	53	23	53	133	220	279	281	350	459	1014	1014	1067	1417	1418	1418	1418	1418	1418	1418	1418	1418	
9.	9.	9.	9.	७.	9.	۰.	9.	9.	9	७.	9.	9.	۰.	9	٠.		9.	٠.	9.	9.	9.	
C4	92	N	N	92	N	2	92	92	92	92	6	92	92	92	92	6	92	92	92	92	92	
20	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20	
24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

#### ALIGNMENTS

Bovine type II collagen peptide (276-288) AAW03105 standard; peptide; 13 AA. (first entry) 03-MAR-1997 AAW03105; AAW0310 

Collagen; type II; Bovine; Human; rheumatoid arthritis; epitope; human major histocompatibility complex; genetically linked. WO9620950-A2 Bos taurus.

96WO-US000206. 04-JAN-1996; 11-JUL-1996.

Rothbard J, Fugger LH, Sonderstrup-Mcdevitt

(IMMU-) IMMULOGIC PHARM CORP.

95US-00369792.

16-JAN-1995;

ö

WPI; 1996-333937/33.

New peptide fragments from human type II collagen - bind to specific major histocompatibility complex proteins and are useful, opt. with known collagen fragments, to treat rheumatoid arthritis.

Claim 1; Page 29; 46pp; English.

The present invention provides peptides, therapeutic compositions, and methods for treatment of rheumatoid arthritis in mammals, specifically in humans. The peptides of the invention comprise fragments of type II collagen which bind specifically with human major histocompatibility complex proteins known to be genetically linked to susceptibility to rheumatoid arthritis. The therapeutic compositions of the invention peptides. AAW03105-107 are claimed peptides which other collagen peptides. AAW03105-107 are claimed peptides which can be used to treat rheumatoid arthritis by down-regulating the autoimmune response, esp. rendering T cells non-responsive to the rheumatoid arthritis-related autoantigen

Sequence 13 AA;

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence represents type II collagen peptide 261-273. The peptide was used in the design of copeptides (see AAY58956-88) that show a high affinity for MHC class II proteins associated with an autoimmune disease, especially HLA-DR1, HLA-DR2 or HLA-DR4, bind to antigen presenting cells, and inhibit T cell responses. The copeptides are used to treat multiple sclerosis, autoimmune haemolytic anaemia, autoimmune oophoritis, autoimmune thrombocytopenic purpura, collis, contact sensitivity disease, diabetes mellitus, Graves disease, Guillain-Barre's syndrome, Hashimoto's disease, idiopathic myxedema, myasthenia gravis, psoriasis, pemphigus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hashimoto's disease; idiopathic myxedema; myasthemia gravis; psoriasis; pemphigus vulgaris; rheumatoid arthritis; systemic lupus erythematosus; lumnosuppressant; neuroprotective; antianaemic; antithyroid; antidiabetic; thyromimetic; antiporiatic; antirheumatic; antiarthritic; dermatological; antifammatory; therapy; major histocompatibility complex; MHC class II; human lymphocyte antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New terpolymers, copeptides and copolymer 1 which contain three amino acids randomly joined in a linear array where one is aromatic, one is aliphatic and the other is charged, used to treat autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 autoimmune haemolytic anaemia; autoimmune oophoritis; autoimmus hyvoiditis; colitis; autoimmune uveoretinitis; colitis; colitis; controli immune thrombocytopenic jurpura; contact sensitivity disease; diabetes mellitus; graves disease; Guillain-Barre's syndrome;
                                                                    Gaps
                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fridkis-Hareli M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Collagen; antigen; autoimmune disease; multiple sclerosis;
   Length 13;
                                                                 1; Indels
   Score 50; DB 2;
Pred. No. 0.044;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sela M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 11; Page 67; 147pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Teitelbaum D, Arnon R,
                                                                                                                                                                                                                                                                                                                                          AAY58994 standard; peptide; 13 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Type II collagen peptide 261-273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEV CO LTD
92.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98US-0101825P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98US-0108184P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99WO-US016747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98US-0093859P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-MAY-2000 (first entry)
   92.6
Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (YEDA ) YEDA RES & DEV (HARD ) HARVARD COLLEGE.
                                                                                                                            1 PKGEQAPKGE 10
                                                                                                                                                                                3 PKGEQGPKGE 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-182641/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200005250-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strominger JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-NOV-1998;
09-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Aharoni R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HLA-DR.
```

```
The present invention describes synthetic peptides having an amino acid sequence comprising at least 3 residues selected from the group of amino acids cacids consisting of aromatic acids, negatively charged amino acids, positively charged amino acids, and aliphatic amino acids, the synthetic positively charged amino acids and aliphatic amino acids, the synthetic peptides being at least 7 amino acid residues in length and capable of binding to a major histocompatibility complex (MHC) class II protein associated with an autorimune disease. The synthetic peptides have anticinflammatory and demyelinating autoimmune diseases, especially rheumatoid arthritis and multiple sclerosis. The peptides are specific for particular MHC class II alleles. Purified, short and synthetic peptides should have fewer side effects than mixtures of random peptides; may include many repeats of the active sequence and/or contain amino acid analogues that improve stability (or other desired features). AAV82041 capresent specifically claimed peptide sequences which can be used as part of the synthetic peptides of the present invention, AAV82045 capable for any and any appeared the synthetic peptides of the present invention, AAV82045 capable for any and any appeared the active sequence of the present invention, AAV82045 capable for any and any appeared the synthetic peptides of the present invention, AAV82045 capable for any appeared as part of the synthetic peptides of the present invention, AAV82045 capable for any and any appeared the and any appropriate and any appropriate and any appropriate and any any appropriate and any appropriate and any appropriate any any and any appropriate and any appropriate and any appropriate any and any appropriate any and any appropriate any and any appropriate any and any appropriate and any appropriate any and any appropriate any and any appropriate any and any appropriate any any any and any appropriate any and any appropriate any and any any appropriate any and any appropriate any any any and any appr
                                                                                                                                                                       ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          peptides from the present invention; and AAY82064 to AAY82080 represent other peptides used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MHC class II; major histocompatibility complex; autoimmune disease; inflammatory disease; binding; rheumatoid arthritis; antiinflammatory; antiarthritic; multiple sclerosis.
                                                                                                                                                                       Gaps
vulgaris, rheumatoid arthritis and systemic lupus erythematosus (all
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New synthetic peptide, useful for treating autoimmune disease, e.g.
                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 3; Length 13;
                                                                                                                      ; DB 3; Length 13;
                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Collagen II (CII) peptide 261-273 SEQ ID NO:2.
                                                                                                                   Score 50; DB 3
Pred. No. 0.044
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92.6%; Score 50;
                                                                                                                                                                                                                                                                                                                                                                                            AAY82065 standard; peptide; 13 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Page 19; 57pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fridkis-Hareli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99WO-US016617.
                                                                                                                   92.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98US-0093859P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry
                                                                                                                                                                       9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HARD ) HARVARD COLLEGE
                                                                                                                                                                                                                     1 FKGEQAPKGE 10
                                                                                                                                                                                                                                                                   12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rheumatoid arthritis.
                                                                                                                                                                                                                                                                   3 FKGEQGPKGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-205374/18
                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strominger JL,
                                                                        Sequence 13 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200005249-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 13 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-FEB-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY82065;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                     AAY82065
ID AAYE
                                                                                                                                                                                                                                                                                                                                           RESULT 3
                                                                                                                                                                                                                        ઠે
                                                                                                                                                                                                                                                                   셤
```

```
APPLICANT: Anaron, kina
APPLICANT: Anaron, kina
APPLICANT: Teitelbaum, Dvora
APPLICANT: Annon, Ruth
APPLICANT: Annon, Ruth
APPLICANT: Sela, Michael
APPLICANT: Eridkis-Harelli, Masha
APPLICANT: Eridkis-Harelli, Masha
APPLICANT: Eridkis-Harelli, Masha
APPLICANT: Eridkis-Harelli, Masha
APPLICANT: Accordinger, Jack
TITLE OF INVENTION: Treatment of Autoimmune Conditions with Copolymer ITLE OF INVENTION: Treatment of Autoimmune Conditions with Copolymer ITLE OF INVENTION: Treatment of Autoimmune Conditions with Copolymer ITLE OF INVENTION: Treatment of Autoimmune Conditions with Copolymer ITLE OF INVENTION WUMBER: US 60/101,825
PRIOR PILING DATE: 1998-01-23
PRIOR PILING DATE: 1998-00-25
PRIOR PILING DATE: 1998-10-30
PRIOR PILING DATE: 1998-10-30
PRIOR PILING DATE: 1998-10-30
PRIOR PILING DATE: 1998-11-12
PRIOR PILING DATE: 1998-11-12
PRIOR PILING DATE: 1998-10-30
PRIOR PILING DATE: 1998-10-30
PRIOR PILING DATE: 1998-10-30
PRIOR PILING DATE: 1999-10-30
                                                                                                                                                                                                                                                                Sequence Seq
                                                                                                                                Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: synthetic peptide (CII amino acids 261-273)
US-09-768-872-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 50; DB 3; Length 13; Pred. No. 0.035; 0; Mismatches 1; Indels
                        US-10-756-149-4739
US-11-202-057-3
US-11-202-057-3
US-11-202-057-7
US-10-194-441A-48
US-10-194-441A-48
US-10-177-293-70
US-10-30-1822-35
US-10-30-1822-35
US-10-36-031B-74
US-10-37-456A-589
US-10-287-436A-589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -10-287-436A-1194
-11-186-284-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/09768872
Patent No. US2002005466A1
GENERAL INFORMATION:
APPLICANT: Aharoni, Rina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 2
US-10-438-538-2
; Sequence 2, Application US/10438538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 90.09; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 FKGEQAPKGE 10
Query Match
Best Local
   8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 124, App Sequence 37, Appl Sequence 59, Appl Sequence 80, Appl Sequence 81, Appl Sequence 78, Appl Sequence 77, Appl Sequence 77, Appl Sequence 61, Appl Sequence 61, Appl Sequence 63, Appl Sequence 79, Appl Sequence 63, Appl Sequence 63, Appl Sequence 79, Appl Sequence 70, Appl Sequence 70,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Appli
Sequence 2, Appli
Sequence 3, Appli
Sequence 27, Appli
Sequence 57, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Published Applications AA Main: *

(EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep: *

(EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep: *

(EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep: *

(EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep: *

(EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep: *

(EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep: *

(EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep: *

(EMC_Celerra_SIDS3/ptodata/2/pubpaa/US111_PUBCOMB.pep: *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                June 23, 2006, 21:25:52; Search time 184 Seconds (without alignments) 25.175 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, A
Sequence 10,
Sequence 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 63,
Sequence 79,
Sequence 15,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seguence
                            GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2097797 segs, 463214858 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     st-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nimum DB seg length: 0 ximum DB seg length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                1 PKGEQAPKGE 10
                                                                                                                                                                                                                                                                                                                                                                       US-10-519-524-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          oring table:
                                                                                                                                                                                                                                                                                                                                                                                                              rfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tabase :
                                                                                                                                                                                                                                                                                                                                                                                                                                              quence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  arched:
```

ö

Gape

```
Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-194-441A-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-194-441A-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-194-441A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ठे
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Strontinger, Jack L.
APPLICANT: Strontinger, Jack L.
APPLICANT: Strontinger, Jack L.
APPLICANT: Strontinger, Jack L.
APPLICANT: STANDARDIN, Masha
TITLE OF INVENTION: Synthetic Peptides and Methods of use for Autoimmune
TITLE OF INVENTION: Disease Therapies
FILE REFERENCE: 24655-013DIV2
CURRENT APPLICATION NUMBER: US/10/438,538
CURRENT FILING DATE: 2003-05-15
PRIOR FILING DATE: 1999-07-22
PRIOR FILING DATE: 1999-07-22
PRIOR FILING DATE: 1999-07-23
PRIOR FILING DATE: 1999-07-23
PRIOR FILING DATE: 1999-03-09
NUMBER OF SEQ ID NOS: 59
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO
Publication No. US20040006022A1
GENERAL INFORMATION:
APPLICANT: Stroninger, Jack L.
APPLICANT: Stroninger, Jack L.
APPLICANT: Stroninger, Jack L.
APPLICANT: Stroninger, Jack L.
APPLICANT: Fridkis-Hareli, Macha
TITLE OF INVENTION: Disease Therapies
FILE DE INVENTION: Disease Therapies
FILE REPRENCE: 24655-013D1V2
CURRENT FILING DATE: 2003-05-15
PRIOR APPLICATION NUMBER: 09/359,099
PRIOR PAPLICATION NUMBER: 60/093,859
PRIOR PILING DATE: 1999-07-22
PRIOR APPLICATION NUMBER: 60/123,675
PRIOR FILING DATE: 1999-03-09
NUMBER OF SEQ ID NOS: 59
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO. 2
LENTH: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PEATURE:
OTHER INFORMATION: Description of Artificial Sequence:Synthetic
OTHER INFORMATION: peptide of predetermined sequence for testing of
OTHER INFORMATION: activity in MHC Class II assays, control collagen
OTHER INFORMATION: II bracketed by alanine residues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92.6%; Score 50; DB 4; Length 13; 90.0%; Pred. No. 0.035;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92.6%; Score 50; DB 4; Length 15; 90.0%; Pred. No. 0.04; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens collagen II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             isULT 3
1-10-438-538-3
Sequence 3, Application US/10438538
Publication No. US20040006022A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 92.6
Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 92.6
Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 FKGEQAPKGE 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 PKGEQGPKGE 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 PKGEQAPKGE 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY: SITE
LOCATION: (1)..(15)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3-10-438-538-2
```

RESULT

PKGEÓGPKGR 13

```
Sequence 6. Application US/1019441A

CHARLICANT: MINIMARY MARCHARD MARCHARD
```

```
à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5028, Ap
Sequence 16938, A
Sequence 16937, A
Sequence 31422, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 47117, A
Sequence 53595, A
Sequence 16936, A
Sequence 54259, A
Sequence 4844, Ap
Sequence 43110, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 27, Appl
Sequence 493, App
Sequence 3, Appli
Sequence 1, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 430, App
Sequence 47117, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 35951,
Sequence 13883,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           / BMC_Celerra_SIDS3/Fcodata/1/pubpaa/US09_NEW_PUB.pep:*
// BMC_Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
// BMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
// BMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
// BMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
// BMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
// BMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
// BMC_Celerra_SIDS3/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                          (without alignments)
10.384 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 25,
Sequence 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                     ; Search time 22 Seconds
GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-11-298-718-1

US-11-298-718-40

US-11-298-718-23

US-11-298-718-26

US-11-298-718-26

US-11-298-718-26

US-11-298-718-26

US-11-298-718-27

US-10-565-570-3

US-10-965-570-3

US-10-965-570-3

US-10-965-570-1

US-10-449-902-31422

US-10-449-902-31422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-953-349-35951
US-10-953-349-13883
                                                                                                                                                                                                                                                                                                                                                                                                                                     tal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Published Applications AA New:*
                                                                                                                                                                                                                                                                                                                                                                                          99297 segs, 22845552 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  st-processing: Minimum Match 0*
Maximum Match 100*
Listing first 45 summaries
                                                                                        - protein search, using sw model
                                                                                                                                                                                                                                                                                                                     BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                  June 23, 2006, 21:26:16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nimum DB seq length: 0 ximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query
Match Length DB
                                                                                                                                                                                                                             US-10-519-524-2
54
                                                                                                                                                                                                                                                                     1 PKGEQAPKGE 10
                                                                                                                                                                                                                                                                                                                     oring table:
                                                                                                                                                                                                                                                       rfect score:
                                                                                          protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tabase :
                                                                                                                                                                                                                                                                            mence:
                                                                                                                                                                                                                                                                                                                                                                                            arched:
```

¥ :	3, A	3, A	4 , e	I, Ap	7, A	IS, A	', Ap	18, A	438, App	11, Appl	6, A	₩, W	14, A	3, A	15, A	. Ap	, A	, A	4, A
3119/	5457	56163	55629	1618		50485	3069,			11,		14195	14194	14193	34935	6151	31496	31495	24974
sednence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence
15-10-449-902-31197	IS-10-449-902-54573	IS-10-449-902-56163	JS-10-449-902-55629	JS-10-471-571A-1618	10-449-902-44467	US-10-449-902-50485	JS-11-293-697-3069	JS-10-449-902-50138	10-505-928-438	11-297-383-11	10-449-902-53956	US-10-953-349-14195	JS-10-953-349-14194	JS-10-953-349-14193	JS-10-449-902-34935	JS-10-953-349-6151	10-953-349-31496	JS-10-953-349-31495	JS-10-953-349-24974
SO	US-	ns-	ns-	us-	US-	ns-	ns-	ns-	ns-	ns-:	ns-	ns-	ns-	ns-	US-	ns-	us-:	ns-:	ns-
٥	v	ø	9	9	9	9	7	ø	9	7	9	v	9	9	9	9	9	9	9
290	290	335	356	390	480	571	621	674	717	883	1279	254	295	364	96	178	187	213	239
59.3	59.3	59.3	59.3	59.3	59.3	59.3	59.3	59.3	59.3	59.3	59.3	58.3	58.3	58.3	57.4	57.4	57.4	57.4	57.4
32	32	32	32	32	32	32	32	32	32	32	32	31.5	31.5	31.5	31	31	31	31	31
26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

### ALIGNMENTS

```
RESULT 1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718-1

19-11-298-718
```

```
Sequence 26, Application US/11298718
Publication No. US200600885441
GENERAL INFORMATION:
APPLICANT: Zimmerman, Daniel
TITLE OF INVENTION: PEPTIDE CONSTRUCTS FOR TREATMENT OF AUTOIMMUNE AND HGV CONDITIONS
FILE REPERENCE: CS-111
CURRENT APPLICATION NUMBER: US/11/298,718
CURRENT FILING DATE: 2002-04-26
RIOR APPLICATION NUMBER: US/10/111,645
PRIOR PILING DATE: 2002-04-26
NUMBER OF SEQ ID NOS: 52
SOFTWARE: Patentin version 3.1
SEQ ID NO 26
LINGTH: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-11-298-718-27

US-11-298-718-27

Sequence 27, Application US/11298718

Publication No. US20060088544A1

GENERAL INFORMATION:

APPLICANT: Zimmerman, Daniel

TITLE OF INVENTION: PEPTIDE CONSTRUCTS FOR TREATMENT OF AUTOIMMUNE AND HGV CONDITIONS

FILE REPERENCE: CS-111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 50; DB 7; Length 33; Pred. No. 0.0031; 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 45; DB 7; Length 14;
Pred. No. 0.011;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: peptide construct
US-11-298-718-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 90.0%;
Matches 9; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83.3%;
                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 PKGEQAPKGE 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24 FKGEQGPKGE 33
22 FKGEQGPKGE 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 FKGEQGPKG 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 PKGEQAPKG 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-11-261-429-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                     SULT 3
Sequence 23, Application US/11298718
GENERAL INFORMATION:
APPLICANT: Zimmerman, Daniel
TITLE OF INVENTION: PEPTIDE CONSTRUCTS FOR TREATMENT OF AUTOIMMUNE AND HGV CONDITIONS
CURRENT FILING DATE: 2005-12-12
PRIOR PILING DATE: 2002-04-26
NUMBER OF SEQ ID NOS: 52
SOFTWARE: Patentin Version 3.1
SEQ ID NO 23
LENGTH: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1-11-298-718-25
Sequence 25, Application US/11298718
Publication No. 2200600885441
GENERAL INFORMATION:
APPLICANT: Zimmerman, Daniel
TITLE OF INVERNION: PEPTIDE CONSTRUCTS FOR TREATMENT OF AUTOIMMUNE AND HGV CONDITIONS
FILE REFERENCE: CS-111
CURRENT APPLICATION NUMBER: US/11/298,718
CURRENT FILING DATE: 2005-12-12
PRIOR APPLICATION NUMBER: US/10/111,645
PRIOR APPLICATION NUMBER: US/10/111,645
NUMBER OF SEQ ID NOS: 52
SOFTWARE: Patentin version 3.1
SEQ ID NO 25
                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 92.6%; Score 50; DB 7; Length 31; Best Local Similarity 90.0%; Pred. No. 0.0029; Matches 9; Conservative 0; Mismatches 1; Indels
                                                                                       Length 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92.6%; Score 50; DB 7; Length 27; 90.0%; Pred. No. 0.0025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . 0.0025;
                                                                                                                            1; Indels
                                                                                         Score 50; DB 7;
Pred. No. 0.0012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: peptide construct:-11-298-718-25
                 FEATURE:
OTHER INFORMATION: peptide construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: peptide construct:-11-298-718-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
ORGANISM: Artificial Sequence
                                                                                       Query Match
Best Local Similarity 90.0%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                 1 FKGEQAPKGE 10
                                                                                                                                                                                                  4 FKGEOGPKGE 13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 PKGEQAPKGE 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 FKGEQAPKGE 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18 FKGEÓGPKGE 27
```

```
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide construct
US-10-111-645A-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 23, Appli
Sequence 25, Appl
Sequence 10, Appl
Sequence 11, Appl
Sequence 11, Appli
Sequence 20, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                    June 23, 2006, 21:13:50 ; Search time 52 Seconds (without alignments) 16.833 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /EMC_celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
/EMC_celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
/EMC_celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
/EMC_celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
/EMC_celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
/EMC_celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
/EMC_celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
/EMC_celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2
Sequence 2
Sequence 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                        650591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-111-645A-27
US-09-795-061-2
US-08-159-339A-816
US-08-159-339A-833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-111-645A-1
US-10-111-645A-40
US-10-111-645A-40
US-10-111-645A-25
US-10-111-645A-25
US-10-111-645A-25
US-10-111-645A-25
US-08-479-722B-10
US-08-479-722B-10
US-08-46B-996-11
US-08-68-996-11
US-08-996-11
                                                                                                                                                                                                                                                                                                                                      tal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                 650591 segs, 87530628 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                          st-processing: Minimum Match 0*
Maximum Match 100*
Listing first 45 summaries
                                                                   - protein search, using sw model
                                                                                                                                                                                                                                              BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patents AA:*
                                                                                                                                                                                                                                                                                                                                                                         nimum DB seq length: 0 ximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
                                                                                                                                                                          US-10-519-524-2
54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1060
                                                                                                                                                                                                           1 FKGEQAPKGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Issued
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query
                                                                                                                                                                                                                                                 oring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score
                                                                                                                                                                                              rfect score:
                                                                     protein
                                                                                                                                                                                                             quence:
                                                                                                                                                                                                                                                                                                     arched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   тараве
```

ស៊

Š

```
%Sequence 23. Application US/10111645A

Sequence 23. Application US/10111645A

Patent No. 6995237

GENERAL INFORMATION:

APPLICANY Zimmerman, Daniel

TITLE OF INVENTION: PEPTIDE CONSTRUCTS FOR TREATMENT OF AUTOIMMUNE AND HGV CONDITIONS

FILE REPERENCE: CS-111

CURRENT PELING DATE: 2002-04-26

NUMBER OF SEQ ID NOS: 52

SOFTWARE: PatentIn version 3.1

SEQ ID NO 23

LENGTH: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92.6%; Score 50; DB 2; Length 27; 90.0%; Pred. No. 0.059;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92.6%; Score 50; DB 5; Length 16; 90.0%; Pred. No. 0.036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: PIPPE: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/00206
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                    CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: KETNEY, ANN-LOUISE
REGISTRATION NUMBER: 33,523
REFERENCE/DOCKET NUMBER: IMZ-014PCT
TELECOMMUNICATION INFORMATION:
TELEFAX: 617-466-6000
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: peptide
PRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Bos taurus type II collagen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ) OTHER INFORMATION: peptide construct
US-10-111-645A-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 25, Application US/10111645A
Patent No. 6995237
GENERAL INFORMATION:
APPLICANT: Zimmerman, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 92.6
Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 FKGEQGPKGE 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 FKGEQAPKGE 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 FKGEQAPKGE 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18 FKGEQGPKGE 27
                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-111-645A-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PCT-US96-00206-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ઠે
                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                              ö
  92.6%; Score 50; DB 2; Length 13; 90.0%; Pred. No. 0.029; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92.6%; Score 50; DB 5; Length 13; 90.0%; Pred. No. 0.029;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABPLICANT: INFORMATION:
APPLICANT: Immunogic Pharmaceutical Corporation
APPLICANT: Immunogic Pharmaceutical Corporation
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: TREATING RHEUMATOID ARTHRITIS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lappin & Kusmer
STREET: 200 State Street
                                                                                                                                                                                                                            Sequence 2, Application PC/TUS9600206
GENERAL INFORMATION:
APPLICANT: ImmuLogic Pharmaceutical Corporation
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: TREATING RHEUMATOID ARTHRITIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/00206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: KERNEY, Ann-Louise
REGISTRATION NUMBER: 33,523
REFERENCE/DOCKET NUMBER: IMZ-014PCT
TELECOMMUNICATION INFORMATION:
TELEFAX: 617-466-6000
TELEFAX: 617-466-6040
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide FRAGMENT TYPE: internal ORIGINAL SOURCE: ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSER: Lappin & Kusmer
STREET: 200 State Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 13 amino acids
  Query Match
Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 92.6
Best Local Similarity 90.0
Matches 9; Conservative
                                                                                   1 FKGEQAPKGE 10
                                                                                                                         4 PKGEQGPKGE 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 PKGEQAPKGE 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 FKGEQGPKGE 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: US
ZIP: 02109
                                                                                                                                                                                      SSULT 3
T-US96-00206-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T-US96-00206-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T-US96-00206-4
```